

Does Not Comply

Corrected Diskette Needed

PCT09

RAW SEQUENCE LISTING DATE: 05/15/2002 PATENT APPLICATION: US/09/673,605A TIME: 15:51:18

Input Set : A:\00246.505003.SEQLIST.TXT
Output Set: N:\CRF3\05152002\1673605A.raw

- 4 <110> APPLICANT: The President and Fellows of Harvard College 6 <120> TITLE OF INVENTION: REGULATION OF BIOFILM FORMATION
- 9 <130> FILE REFERENCE: 00246/505003
- 11 <140> CURRENT APPLICATION NUMBER: 09/673,605A
- 12 <141> CURRENT FILING DATE: 2000-10-17
- 14 <150> PRIOR APPLICATION NUMBER: 60/102,870
- 15 <151> PRIOR FILING DATE: 1998-10-02
- 17 <150> PRIOR APPLICATION NUMBER: 60/083,259
- 18 <151> PRIOR FILING DATE: 1998-04-27
- 20 <160> NUMBER OF SEQ ID NOS: 49
- 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0

ERRORED SEQUENCES

- 690 <210> SEQ ID NO: 34
- 691 <211> LENGTH: 595
- 692 <212> TYPE: PRT
- 693 <213> ORGANISM: Escherichia coli
- 695 <400> SEQUENCE: 34
- 696 Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Ile Thr Gln Asn
- E--> 697 1 5 10 15 698 Asn Ile Asn Lys Asn Gln Ser Ala Leu Ser Ser Ser Ile Glu Arg Leu
 - 699 20 25 30
 - 700 Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Gln
 701 35 40 45
 - 702 Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala
 - 703 50 55
 - 704 Ala Arg Asn Ala Asn Asp Gly Ile Ser Val Ala Gln Thr Thr Glu Gly
 - 705 65 70 75 80 706 Ala Leu Ser Glu Ile Asn Asn Leu Gln Arg Ile Arg Glu Leu Thr
 - 707 85 90 95
 - 708 Val Gln Ala Ser Thr Gly Thr Asn Ser Asp Ser Asp Leu Asp Ser Ile 709 100 105 110
 - 710 Gln Asp Glu Ile Lys Ser Arg Leu Asp Glu Ile Asp Arg Val Ser Gly 711 115 120 125
 - 712 Gln Thr Gln Phe Asn Gly Val Asn Val Leu Ala Lys Asp Gly Ser Met
 - 713 130 135 140 714 Lys Ile Gln Val Gly Ala Asn Asp Gly Gln Thr Ile Thr Ile Asp Leu
 - 715 145 150 155 160 716 Lys Lys Ile Asp Ser Asp Thr Leu Gly Leu Asn Gly Phe Asn Val Asn

 - 718 Gly Ser Gly Thr Ile Ala Asn Lys Ala Ala Thr Ile Ser Asp Leu Thr



Input Set : A:\00246.505003.SEQLIST.TXT Output Set: N:\CRF3\05152002\1673605A.raw

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722	Ala	Leu	Thr	Ala	Ser	Lys		Leu	Asp	Gln	Leu		Asp	Gly	Asp	Thr
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724	Val	Thr	Ile	Lys	Ala	Asp	Ala	Ala	Gln	Thr	Ala	Thr	Val	Tyr	Thr	Tyr
725	225					230					235					240
726	Asn	Ala	Ser	Ala	Gly	Asn	Phe	Ser	Phe	Ser	Asn	Val	Ser	Asn	Asn	Thr
727					245					250					255	
728	Ser	Ala	Lys	Ala	Gly	Asp	Val	Ala	Ala	Ser	Leu	Leu	Pro	Pro	Ala	Gly
729			-	260	-	-			265					270		-
	Gln	Thr	Ala		Gly	Va l	Tvr	Lvs	Ala	Ala	Ser	Glv	Glu	Val	Asn	Phe
731	0.2		275		1		-1-	280				- _1	285			
	Δen	Va 1		Δla	Asn	Glv	Lvc		Thr	Tle	Glv	G1 v		Glu	Δla	Tvr
733	изБ	290	пор	nia	. ASII	OLY	295	110	1111	110	GLY	300	OIII	Olu	1114	-1-
	T 011		Cor	7 an	Gly	7 an		Thr	mb ~	λαn	7 an		C1,,	C1 77	λla	Thr
		TIII	ser	ASP	СТУ		Leu	TIII	1111	ASII		нта	СТУ	СТУ	Ата	
	305		m1	_		310	. .	51. -	T	.	315	a 1	3	a 1	01-	320
	Ala	Ата	Thr	Leu	Asp	GIY	ьeu	Pne	ьys	_	Ата	GIY	Asp	GIY		ser
737				_	325		_ •	_		330					335	_
	Ile	GTA	Phe		Lys	Thr	Ala	Ser		Thr	Met	GLY	GTA		Thr	Tyr
739				340					345					350		
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741			355					360					365			
742	Val	Ser	Phe	Thr	Asp	Thr	Ala	Ser	Lys	Glu	Thr	Val	Leu	Asn	Lys	Val
743		370					375					380				
744	Ala	Thr	Ala	Lys	Gln	Gly	Thr	Ala	Val	Ala	Ala	Asn	Gly	Asp	Thr	Ser
745	385					390					395					400
746	Ala	Thr	Ile	Thr	Tyr	Lys	Ser	Gly	Val	Gln	Thr	Tyr	Gln	Ala	Val	Phe
747					405	•		-		410		-			415	
748	Ala	Ala	Glv	Asp	Gly	Thr	Ala	Ser	Ala	Lvs	Tvr	Ala	Asp	Asn	Thr	Asp
749				420	2				425	4	•		- 1	430		•
	Va 1	Ser	Asn		Thr	Ala	Thr	Tvr	Thr	Asp	Ala	Asp	Glv	Glu	Met	Thr
751		001	435					440					445	014		
	Thr	Tla		Sar	Tyr	Thr	Thr		Tur	Sar	Tlo	Δen		Δen	Δcn	Clv
753	1111	450	O _T	OCI	- 7 -	T 11.T	455	בעם	- 1 -	DCI	110	460	71.LU	11511	11511	OI1
	Two		Πh∞	Wa 1	Asp	Cor		mh.r	C1++	Cor	C111		Пттт	λla	Dro	Tvc
	_	Val	1111	val	ASP	470	GIY	1111	GIY	Set	475	цуѕ	тут	Ата	PIU	480
	465	01	7 1 n	C1	17n 1		17- 1	C	3 1 n	7.00		mh m	T 0	mh-s	mhm	
	vaı	GIY	Ата	GIU	Val	туг	vaı	ser	Ата		СТА	Thr	Leu	Thr		ASP
757			_		485	_,			_	490	_	_	_		495	_
	Ala	Thr	Ser		Gly	Thr	Val	Thr	_	Asp	Pro	Leu	ьуs		Leu	Asp
759				500					505					510		_
	Glu	Ala		Ser	Ser	Ile	Asp	_	Phe	Arg	Ser	Ser		Gly	Ala	Ile
761			515					520					525			
762	Gln	Asn	Arg	Leu	Asp	Ser	Ala	Val	Thr	Asn	Leu	Asn	Asn	Thr	Thr	Thr
763		530					535					540				
764	Asn	Leu	Ser	Glu	Ala	Gln	Ser	Arg	Ile	Gln	Asp	Ala	Asp	Tyr	Ala	
765	545					550					555					560
766	Glu	Val	Ser	Asn	Met	Ser	Lys	Ala	Gln	Ile	Ile	Gln	Gln	Ala	Gly	Asn
767					•		_								_	

570

575 g Ser Val Leu Ala Lys Ala Asn Gln issert Land return

565

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                                             10
     777 Asn Leu Ser Tyr Leu Leu Leu Ala Gln Arg Leu Ile Val Gln Asp Lys
                     20
                                         25
     779 Ala Ser Ala Met Phe Arg Leu Gly Ile Asn Glu Glu Met Ala Thr Thr
     781 Leu Ala Ala Leu Thr Leu Pro Gln Met Val Lys Leu Ala Glu Thr Asn
     783 Gln Leu Val Cys His Phe Arg Phe Asp Ser His Gln Thr Ile Thr Gln
     785 Leu Thr Gln Asp Ser Arg Val Asp Asp Leu Gln Gln Ile His Thr Gly
                85
                                    90
                                                        95 🥂 Ile Met Leu Ser Thr Arg Leu Leu
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     790 <212> TYPE: PRT
     791 <213> ORGANISM: Escherichia coli
     793 <400> SEQUENCE: 36
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     796 Gly Tyr Leu Met Thr Gly Gly Ser Leu Gly Ala Leu Tyr Gln Pro Ala
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     798 Glu Leu Val Ile Ile Ala Gly Ala Gly Ile Gly Ser Phe Ile Val Gly
     800 Asn Asn Gly Lys Ala Ile Lys Gly Thr Leu Lys Ala Leu Pro Leu Leu
                                 55
     802 Phe Arg Arg Ser Lys Tyr Thr Lys Ala Met Tyr Met Asp Leu Leu Ala
                             70
     804 Leu Leu Tyr Arg Leu Met Ala Lys Ser Arg Gln Met Gly Met Phe Ser
E--> 806 Leu Glu Arg Asp Ile Glu Asn Pro Arg Glu Ser Glu Ile Phe Ala Ser
     807 100
                                        105
     808 Tyr Pro Arg Ile Leu Ala Asp Ser Val Met Leu Asp Phe Ile Val Asp
                                    120
     810 Tyr Leu Arg Leu Ile Ile Ser Gly His Met Asn Thr Phe Glu Ile Glu
                                 135
     812 Ala Leu Met Asp Glu Glu Ile Glu Thr His Glu Ser Glu Ala Glu Val
     813 145
                             150
                                                 155
     814 Pro Ala Asn Ser Leu Ala Leu Val Gly Asp Ser Leu Pro Ala Phe Gly
                         165
                                             170
     816 Ile Val Ala Ala Val Met Gly Val Val His Ala Leu Gly Ser Ala Asp
                     180
                                        185
     818 Arg Pro Ala Ala Glu Leu Gly Ala Leu Ile Ala His Ala Met Val Gly
                                    200
     820 Thr Phe Leu Gly Ile Leu Leu Ala Tyr Gly Phe Ile Ser Pro Leu Ala
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DATE: 05/15/2002

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PATENT APPLICATION: US/09/673,605A
                                                             TIME: 15:51:19
                     Input Set : A:\00246.505003.SEQLIST.TXT
                     Output Set: N:\CRF3\05152002\1673605A.raw
     821
             210
                                 215
     822 Thr Val Leu Arg Gln Lys Ser Ala Glu Thr Ser Lys Met Met Gln Cys
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                                                 235
     824 Val Lys Val Thr Leu Leu Ser Asn Leu Asn Gly Tyr Ala Pro Pro Ile
                                             250
                         245
     826 Ala Val Glu Phe Gly Arg Lys Thr Leu Tyr Ser Ser Glu Arg Pro Ser
E--> 827
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                                                              Phe Ile Glu Leu Glu Glu His Val
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     831 <212> TYPE: PRT
     832 <213> ORGANISM: Escherichia coli
     834 <400> SEQUENCE: 37
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     839 Phe Met Thr Ala Met Met Ala Phe Phe Leu Val Met Trp Leu Ile Ser
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                                     40
     841 Ile Ser Ser Pro Lys Glu Leu Ile Gln Ile Ala Glu Tyr Phe Arg Thr
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     843 Pro Leu Ala Thr Ala Val Thr Gly Gly Asp Arg Ile Ser Asn Ser Glu
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                                                 75
     845 Ser Pro Ile Pro Gly Gly Gly Asp Asp Tyr Thr Gln Ser Gln Gly Glu
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                                             90
     847 Val Asn Lys Gln Pro Asn Ile Glu Glu Leu Lys Lys Arg Met Glu Gln
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                     100
                                         105
     849 Ser Arg Leu Arg Lys Leu Arg Gly Asp Leu Asp Gln Leu Ile Glu Ser
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                                     120
     851 Asp Pro Lys Leu Arg Ala Leu Arg Pro His Leu Lys Ile Asp Leu Val
                                135
     853 Gln Glu Gly Leu Arg Ile Gln Ile Ile Asp Ser Gln Asn Arg Pro Met
                            150
                                                 155
     855 Phe Arg Thr Gly Ser Ala Asp Val Glu Pro Tyr Met Arg Asp Ile Leu
                         165
                                             170
     857 Arg Ala Ile Ala Pro Val Leu Asn Gly Ile Pro Asn Arg Ile Ser Leu
                    180
                                         185
     859 Ser Gly His Thr Asp Asp Phe Pro Tyr Ala Ser Gly Glu Lys Gly Tyr
                                     200
     861 Ser Asn Trp Glu Leu Ser Ala Asp Arg Ala Asn Ala Ser Arg Arg Glu
                                 215
    863 Leu Met Val Gly Gly Leu Asp Ser Gly Lys Val Leu Arg Val Val Gly
                             230
    864 225
                                                 235
     865 Met Ala Ala Thr Met Arg Leu Ser Asp Arg Gly Pro Asp Asp Ala Val
                         245
                                             250
     867 Asn Arg Arg Ile Ser Leu Leu Val Leu Asn Lys Gln Ala Glu Gln Ala
                     260
                                         265
E--> 869 Ile Leu His Glu Asn Ala Glu Ser Gln Asn Glu Pro Val Ser Ala Leu
E--> 870 💉 🕡
       275
                            280
                                                285
                                                               Glu Lys Pro Glu Val Ala Pro Gln
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RAW SEQUENCE LISTING

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                                         25
     882 Gly Gly Gly Gln Ser Trp Ser Leu Pro Val Gln Thr Leu Val Phe Ile
     884 Thr Ser Leu Thr Phe Ile Pro Ala Ile Leu Leu Met Met Thr Ser Phe
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     887 65
     888 Pro Ser Ala Pro Pro Asn Gln Val Leu Leu Gly Leu Ala Leu Phe Leu
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     890 Thr Phe Phe Ile Met Ser Pro Val Ile Asp Lys Ile Tyr Val Asp Ala
                     100
                                         105
     892 Tyr Gln Pro Phe Ser Glu Glu Lys Ile Ser Met Gln Glu Ala Leu Glu
                 115
                                     120
     894 Lys Gly Ala Gln Pro Leu Arg Glu Phe Met Leu Arg Gln Thr Arg Glu
                                 135
     896 Ala Asp Leu Gly Leu Phe Ala Arg Leu Ala Asn Thr Gly Pro Leu Gln
     898 Gly Pro Glu Ala Val Pro Met Arg Ile Leu Leu Pro Ala Tyr Val Thr
     900 Ser Glu Leu Lys Thr Ala Phe Gln Ile Gly Phe Thr Ile Phe Ile Pro
     901
                     180
                                         185
     902 Phe Leu Ile Ile Asp Leu Val Ile Ala Ser Val Leu Met Ala Leu Gly
                                     200
     904 Met Met Met Val Pro Pro Ala Thr Ile Ala Leu Pro Phe Lys Leu Met
E--> 905
                                            220
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     915 Leu Pro Gly Gly Lys Ala Ser Asp Ala Ala Gln Asp Phe Leu Ala Leu
     917 Leu Ser Glu Ala Leu Ala Gly Glu Thr Thr Thr Asp Lys Ala Ala Pro
                                     40
     919 Gln Leu Leu Val Ala Thr Asp Lys Pro Thr Thr Lys Gly Glu Pro Leu
     921 Ile Ser Asp Ile Val Ser Asp Ala Gln Gln Ala Asn Leu Leu Ile Pro
     923 Val Asp Glu Thr Pro Pro Val Ile Asn Asp Glu Gln Ser Thr Ser Thr
     924
                         85
                                             90
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DATE: 05/15/2002

TIME: 15:51:19

Input Set : A:\00246.505003.SEQLIST.TXT Output Set: N:\CRF3\05152002\1673605A.raw 925 Pro Leu Thr Thr Ala Gln Thr Met Ala Leu Ala Ala Val Ala Asp Lys 100 105 927 Asn Thr Thr Lys Asp Glu Lys Ala Asp Asp Leu Asn Glu Asp Val Thr 115 120 929 Ala Ser Leu Ser Ala Leu Phe Ala Met Leu Pro Gly Phe Asp Asn Thr 130 135 140 931 Pro Lys Val Thr Asp Ala Pro Ser Thr Val Leu Pro Thr Glu Lys Pro 150 155 933 Thr Leu Phe Thr Lys Leu Thr Ser Glu Gln Leu Thr Thr Ala Gln Pro 165 170 935 Asp Asp Ala Pro Gly Thr Pro Ala Gln Pro Leu Thr Pro Leu Val Ala 185 937 Glu Ala Gln Ser Lys Ala Glu Val Ile Ser Thr Pro Ser Pro Val Thr 195 200 939 Ala Ala Ala Ser Pro Leu Ile Thr Pro His Gln Thr Gln Pro Leu Pro 215 220 E--> 941 Thr Val Ala Ala Pro Val Leu Ser Ala Pro Leu Gly Ser His Glu Trp 230 235 943 Gln Gln Ser Leu Ser Gln His Ile Ser Leu Phe Thr Arg Gln Gly Gln 250 245 945 Gln Ser Ala Glu Leu Arg Leu His Pro Gln Asp Leu Gly Glu Val Gln 260 265 947 Ile Ser Leu Lys Val Asp Asp Asn Gln Ala Gln Ile Gln Met Val Ser 280 949 Pro His Gln His Val Arg Ala Ala Leu Glu Ala Ala Leu Pro Val Leu 951 Arg Thr Gln Leu Ala Glu Ser Gly Ile Gln Leu Gly Gln Ser Asn Ile 952 305 310 315 953 Ser Gly Glu Ser Phe Ser Gly Gln Gln Ala Ala Ser Gln Gln Gln 330 955 Gln Ser Gln Arg Thr Ala Asn His Glu Pro Leu Ala Gly Glu Asp Asp E--> 956 340 345 Asp Thr Leu Pro Val Pro Val Ser 958 <210> SEQ ID NO: 40 959 <211> LENGTH: 547 same 960 <212> TYPE: PRT 961 <213> ORGANISM: Escherichia coli 963 <400> SEQUENCE: 40 964 Met Ser Ser Leu Ile Asn Asn Ala Met Ser Gly Leu Asn Ala Ala Gln 966 Ala Ala Leu Asn Thr Ala Ser Asn Asn Ile Ser Ser Tyr Asn Val Ala 20 25 968 Gly Tyr Thr Arg Gln Thr Thr Ile Met Ala Gln Ala Asn Ser Thr Leu 40 970 Gly Ala Gly Gly Trp Val Gly Asn Gly Val Tyr Val Ser Gly Val Gln 972 Arg Glu Tyr Asp Ala Phe Ile Thr Asn Gln Leu Arg Ala Ala Gln Thr 70 75 974 Gln Ser Ser Gly Leu Thr Ala Arg Tyr Glu Gln Met Ser Lys Ile Asp

90

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/673,605A

85

975

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		Phe	Phe	Thr 115	Ser	Leu	Gln	Thr	Leu 120	Val	Ser	Asn	Ala	Glu 125	Asp	Pro	Ala
		Ala	Arg 130		Ala	Leu	Ile	Gly 135		Ser	Glu	Gly	Leu 140		Asn	Gln	Phe
		Lvs		Thr	Δen	Gln	Tvr		Δrσ	Δsn	Gln	Δsn		Gln	Val	Asn	Tle
	983	_	1111	1111	пор	OIII	150	пси	111.9	пор	0	155	D 10	0.1.11	, 41		160
			Ile	Gly	Ala	Ser 165		Asp	Gln	Ile	Asn 170		Tyr	Ala	Lys	Gln 175	
		Ala	Ser	Len	Asn		Gln	Tle	Ser	Ara		Thr	Glv	Val	Gly		Glv
	987				180					185			1		190		1
	988 989	Ala	Ser	Pro 195	Asn	Asn	Leu	Leu	Asp 200	Gln	Arg	Asp	Gln	Leu 205	Val	Ser	Glu
		Leu	Asn	Gln	Ile	Val	Gly	Val		Val	Ser	Val	Gln	Asp	Gly	Gly	Thr
	991		210				_	215					220	_	_	_	
		_	Asn	Ile	Thr	Met	Ala	Asn	Gly	Tyr			Val	Gln	Gly	Ser	Thr
	993			_		_	230	_				235					240
		Ala	Arg	Gln	Leu		Ala	Val	Pro	Ser		Ala	Asp	Pro	Ser		Thr
	995	Пhт	17-1	x 1 -	m	245	7.00	C1	mb~	3.1 a	250	A an	т1.	C1	тlä	255	Clu
	990	TIIT	Val		260	vaı	ASP	СТА	1111	265	GIĀ	ASII	TIE	GIU	Ile 270	PIO	Giu
		Lvs	Leu			Thr	Glv	Ser	Leu		Glv	Ile	Leu	Thr	Phe	Ara.	Ser
	999	-1-		275			V-1		280	1	1			285		,	
	1000	Gln	Asp	Leu	Asp	Gln	Thr	Arg	Asn	Thr	Leu	Gly	Gln	Leu	Ala	Leu	Ala
	1001		290					295					300				
				Glu	Ala	Phe			Gln	His	Lys			Phe	Asp	Ala	Asn
	1003			. 7.1.	C1.		310		nho	. או	т1.	315		Dr.o	. או	37 - 1	320 Leu
	1004		ASP	ніа	СТУ	325		Pile	: PHE	нта	330		пуз	PIC	ИТО	335	
			Asn	Thr	Lvs			Glv	Asp	Val			Glv	Ala	Thr		Thr
	1007				340		_1 -	1	1	345					350		
E>	1008	Asp	Ala	Ser	Ala	Val	Leu	Ala	Thr	Asp	Tyr	Lys	Ile	Ser	Phe	Asp	Asn
	1009		_	355		_			360				_	365			•
				_	Gln	Val	Thr	_		. Ala	Ser	Asn			Phe	Thr	Val
	1011		370		λla	λen	G1v	375		λla	Dho	λen	380		Glu	T.e.n	Thr
	1013			nsp	MIG	. ASI	390	_	Val	ALU		395	_	БСС	. OIu	DC u	400
				Gly	Thr	Pro			Asn	Asp	Ser	-		Leu	Lys	Pro	Val
	1015			_		405	ı			_	410					415	
			Asp	Ala			Asn	Met	Asp			Ile	Thr	Asp			Lys .
	1017				420				_	425		_	_	_	430		_
	1018		АІа			Ser	Glu	Glu	_		GLY	Asp	Ser	Asp 445		Arg	Asn
			Gln	435 Ala		T.Ou	λen	T.Qu	440		λen	Sar	Luc			Glv	Gly
	1021		450		Leu	леи	nap	455		Det	nou	Der	460		, u I	СТУ	OLY.
					Phe	Asn	Asp			Ala	Ser	Leu			Asp	Ile	Gly
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RAW SEQUENCE LISTING

DATE: 05/15/2002 TIME: 15:51:19

PATENT APPLICATION: US/09/673,605A

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1025
                          485
     1026 Val Thr Gln Leu Ser Asn Gln Gln Ser Ile Ser Gly Val Asn Leu
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                     500
     1028 Asp Glu Glu Tyr Gly Asn Leu Gln Arg Phe Gln Gln Tyr Tyr Leu Ala
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     1047 Ala Ile Ser Glu Lys Leu Val Arg Gln His Arg Val Ile Pro Leu Trp
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                         85
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     1051 Gln Ala Ile Asn Asp Val Gln Phe Ser Thr Gly Leu Thr Thr Glu Ala
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                                      120
     1053 Ile Leu Val Glu Asp Asp Lys Leu Gly Leu Ala Ile Asp Lys Leu Phe
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                                  135
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     1085 Leu Arg Gln Asp Pro Asp Val Ile Met Val Gly Glu Ile Arg Asp Leu
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                                                  395
     1087 Glu Thr Ala Glu Ile Ala Ile Lys Ala Ala Gln Thr Gly His Met Val
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     1089 Met Ser Thr Leu His Thr Asn Ser Ala Ala Glu Thr Leu Thr Arg Leu
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    1091 Leu Asn Met Gly Val Pro Ala Phe Asn Leu Ala Thr Ser Val Asn Leu
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    1093 Ile Ile Ala Gln Arg Leu Ala Arg Lys Leu Cys Ser His Cys Lys
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    1095 Glu His Asp Val Pro Lys Glu Thr Leu Leu His Glu Gly Phe Pro Glu
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    1097 Glu Leu Ile Gly Thr Phe Lys Leu Tyr Ser Pro Val Gly Cys Asp His
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    1101 Asn Thr Pro Ala Leu Gln Arg Ile Ile Met Glu Glu Gly Asn Ser Ile
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E--> 1103 Glu Ile Ala Glu Gln Ala Arg Lys Glu Gly Phe Asn Asp Leu Arg Thr
E--> 1104
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    1122 Ala Gly Val Pro Leu Gln Ser Phe Asp Ile Ile Gly Glu Gly Phe
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    1124 Asp Asn Pro Asn Met Arg Lys Leu Val Asp Glu Ile Lys Gln Glu Val
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    1126 Ser Ser Gly Asn Ser Leu Ala Asn Ser Leu Arg Lys Lys Pro Gln Tyr
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     1128 Phe Asp Glu Leu Tyr Cys Asn Leu Val Asp Ala Gly Glu Gln Ser Gly
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     1130 Ala Leu Glu Asn Leu Leu Asp Arg Val Ala Thr Tyr Lys Glu Lys Thr
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     1136 Val Pro Gln Phe Gln Ser Val Phe Glu Gly Phe Gly Ala Glu Leu Pro
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     1138 Ala Phe Thr Gln Met Ile Val Asn Leu Ser Glu Phe Met Gln Glu Trp
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     1140 Trp Phe Phe Ile Ile Leu Ala Ile Ala Ile Phe Gly Phe Ala Phe Lys
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     1141 225
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    1148 Leu Val Asp Ala Leu Asp Ser Val Ser Gly Ala Thr Gly Asn Ile Val
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                                                     300
    1150 Phe Lys Asn Ala Val Ser Lys Ile Lys Gln Asp Val Ser Thr Gly Met
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    1152 Gln Leu Asn Phe Ser Met Arg Thr Thr Ser Val Phe Pro Asn Met Ala
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                                         345
    1156 Leu Ser Lys Val Ala Ser Tyr Tyr Glu Glu Glu Val Asp Asn Ala Val
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∧ Val Leu Val Gly Gly Leu Ile Val

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    1171 Val His Arg Leu Pro Lys Met Met Glu Arg Asn Trp Lys Ala Glu Ala
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    1173 Arg Glu Ala Leu Gly Leu Glu Pro Glu Pro Lys Gln Ala Thr Tyr Asn
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    1175 Leu Val Leu Pro Asn Ser Ala Cys Pro Arg Cys Gly His Glu Ile Arg
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     1179 Cys Ser Ser Cys Lys Ala Ala Ile Gly Lys Arg Tyr Pro Leu Val Glu
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                                      120
     1183 Thr Trp Gln Ala Gly Ala Met Leu Leu Leu Thr Trp Gly Leu Leu Ala
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     1185 Met Ser Leu Ile Asp Ala Asp His Gln Leu Leu Pro Asp Val Leu Val
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     1189 Ala Ser Leu Asp Asp Ala Leu Phe Gly Ala Val Phe Gly Tyr Leu Ser
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     1191 Leu Trp Ser Val Phe Trp Leu Phe Lys Leu Val Thr Gly Lys Glu Gly
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     1193 Met Gly Tyr Gly Asp Phe Lys Leu Leu Ala Met Leu Gly Ala Trp Gly
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     1195 Gly Trp Gln Ile Leu Pro Leu Thr Ile Leu Leu Ser Ser Leu Val Gly
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                                                  235
     1197 Ala Ile Leu Gly Val Ile Met Leu Arg Leu Arg Asn Ala Glu Ser Gly
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     1199 Thr Pro Ile Pro Phe Gly Pro Tyr Leu Ala Ile Ala Gly Trp Ile Ala
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     1212 Gly Met Ile Ala Met Gln Gly Lys Thr Ile Gln Tyr Thr Ala Asp Ser
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     1214 Val Glu Arg Asn Lys Ala Ala Met Leu Gly Ser Asn Leu Leu Glu Ser
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     1216 Met Arg Ala Ser Pro Lys Ala Leu Tyr Asp Val Lys Asp Gln Met Ala
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     1222 Cys Trp Ala Glu Gln Val Lys Asn Glu Leu Pro Gly Ala Gly Asp Leu
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     1224 Leu Lys Ser Asp Tyr Tyr Ile Cys Arg Ser Ser Lys Pro Gly Asp Cys
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     1226 Asp Gly Lys Gly Ser Met Leu Glu Ile Arg Leu Ala Trp Arg Gly Lys
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    1238 Glu Leu Leu Val Ala Leu Ala Ile Ser Ser Phe Leu Ile Leu Gly Ile
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    1240 Thr Gln Ile Tyr Leu Asp Asn Lys Arg Asn Tyr Leu Phe Gln Gly
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     1242 Gln Ala Gly Asn Gln Glu Asn Gly Arg Phe Ala Met Met Phe Leu Asp
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    1246 Glu Phe Ala Phe Pro Ala Gln Gln Lys Thr Ala Tyr Cys Glu Ala Phe
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                                        105
    1250 Gly Phe Cys Tyr Arg Tyr Gln Pro Ala Pro Gly Glu Ala Tyr Asp Cys
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    1252 Glu Gly Asn Ser Ile Thr Thr Pro Ser Asp Pro Phe Ala Thr Ala Gln
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    1254 Ala Ile Thr Ala Arg Val Leu Phe Val Pro Ala Thr Ala Asp Val Pro
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    1256 Gly Ser Leu Ala Cys Ser Ala Gln Thr Ile Lys Glu Lys Gly Gln Glu
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                                             170
    1258 Ile Val Ser Gly Leu Val Asp Phe Lys Leu Glu Tyr Gly Val Gly Pro
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                    180
    1260 Thr Met Ala Gly Lys Arg Glu Val Glu Ser Phe Val Glu Gln Ala Asn
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                                                     220
    1264 Ser Asp Lys Asn Leu Arg Gln Gly Asp Ser Lys Thr Leu Asp Asp Trp
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                                                 235
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     1283 Phe Val Asn Thr Leu Arg Pro Pro Glu Pro Gly Thr Gly Cys Thr Ala
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     1289 Ala Asn Thr Trp Met Ser Tyr Arg Gly Ser Asp Ile Ser Ser Ala Thr
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     1305 Leu Tyr Gln Leu Ile Glu Pro Arg Met Lys Ser Val Leu His Gln Ile
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     1309 Ala Gln Thr Thr His Ala Ala Ala Leu Ser Val Ser Gln Gln Pro Leu
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                                          105
     1315 Gly Asn Tyr Thr Phe Phe Ala Ser Asn Ser Phe Asn Pro Met Tyr Phe
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                                  135
                                                      140
    1319 Gly Gln Val Gln Ile Gln Asp Tyr Pro Ala Pro Asn Phe Ser Ser Ala
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    1323 Tyr Lys Val Thr Ile Glu Tyr Gly Arg Gly Tyr Asp Lys Glu Ser Thr
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                                  215
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1341 1342	Glu	Ala	Ser	Phe	Ser 325	Arg	Arg	Pro	Ala	Ser 330	Asn	Gly	Pro	Tyr	Ala 335	Tyr
1343 1344	Arg	Pro	Gly	Thr 340	Gln	Thr	Ala	Pro	Glu 345	Tyr	Ser	Cys	Arg	Gly 350	Ser	Tyr
1345 1346	His	Ile	Leu 355	Met	Thr	Asp	Gly	Leu 360	Trp	Asn	Asn	Asp	Ser 365	Ala	Asn	Val
1347 1348	Gly	Asn 370	Ala	Asp	Ser	Thr	Ala 375	Arg	Asn	Leu	Pro	Asp 380	Gly	Lys	Ser	Tyr
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1367 1368	Ile	Ser 530	Gly	Lys	Asp	Leu	Pro 535	Ala	Ser	Arg	Pro	Ala 540	Ile	Ser	Ser	Ser
1369 1370		Gln	Glu	Asp	Asp	Thr 550	Gly	Asp	Lys	Leu	Thr 555	Arg	Phe	Ala	Tyr	Gln 560
1371 1372	Thr	Ser	Phe	Ala	Ser 565	_	Lys	Asn		Ala 570		Asp	Leu	Thr	Arg 575	
1373 1374	Ser	Leu	Thr	Thr 580	Gln	Asp	Lys	Ala	Thr 585	Val	Gln	Thr	Asn	Leu 590	Trp	Ser
1375 1376	Ala	Gln	Ser 595		Leu	Asp	Ala	Met 600		Asn	Gly	Gly	Ala 605	Gly	Arg	Lys
1377 1378	Ile	Met 610		Ala	Gly	Ser	Gly 615		Ser	Gly	Leu	Lys 620		Phe	Thr	Trp
1379 1380			Leu	Ser	Ala	Asp 630		Gln	Arg	Lys	Leu 635		Arg	Asp	Pro	Asp 640
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1391	Val	Gly	Ala	Asn	Asp	Gly	Met	Leu	His	Gly	Phe	Asp	Thr	Asp	Gly	Asn
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1401	Asp	Val	Thr	Asp		Ala	Asn	тте	Lys		Leu	Trp	GIU	тте		vaı
1402		a1	a 1	D	805	T	01	m	a	810	D	T	D	m l	815	310
1403	Asp	GIN	GIU		Asp	Leu	GTĀ	Tyr	825	Pne	Pro	ьуs	Pro	830	vaı	Ala
1404 1405	3	т о	mi a	820	C1	Tira	m~n	ת 1 ת		37 - 3	Пhъ	C1**	7 an		mazz	Sor
	Arg	Leu	835	ASII	СТУ	гуѕ	пр	840	vai	val	1111	GIY	845	GIY	тут	ser
1406 1407	Car	Lou		λen	Lve	λla	λla		T.Q11	Tla	Tlo	Δen		Glu	Thr	Glv
1407	ser	850	ASII	ASP	гуэ	АІа	855	Бец	Бец	116	116	860	пец	GIU	T 111	GLY
1409	Δla		Thr	Ara	T.vs	T.eu		Va1	Thr	Glv	Arσ		Glv	Va l	Pro	Asn
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1423	Ile	Phe	GLY		Gly	Lys	Tyr	Phe		Asn	Ala	Asp	Ala		АТа	Asp
1424	1	_	_	980	a 1.	ml	+		985	T1-	m	3	a1	990	m1	T
1425	Thr	ser	-	Ата	GIN	Thr	ьeu			тте	Trp	Asp			rnr	гàг
1426 1427	C1**	Clu	995	7 J ¬		C02	πh∽	1000		Len	ሞኮም	λνα	1005		Len	Gla
	ату	1010		нта	ату	per	1015		Ary	neu	TIII	1020		Maii	Leu	GTII
1428 1429	Gln			T.eu	λερ	T.eu			Δen	Ser	Thr			Ser	Thr	Δla
1430			T 11T	шeu	vah	1030		ALU	чэр	JUL	1035		лти	JUI	1111	104
		-					•					-			`	رنت
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E-->

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     1436 1075
                                     1080
     1437 Gln Val Val Leu Leu Gln Thr Ile Thr Pro Asn Asp Asp Pro Cys Ala
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                                 1095
                                                      1100
     1439 Asp Gly Ala Ser Asn Trp Thr Tyr Gly Leu Asp Pro Tyr Thr Gly Gly
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RAW SEQUENCE LISTING

DATE: 05/15/2002

PATENT APPLICATION: US/09/673,605A

TIME: 15:51:19

115

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Cys Gly Lys Leu Thr Leu Asn Gln Leu Gly Glu Arg Gly Ala Ala Gly

120

VERIFICATION SUMMARY DATE: 05/15/2002 PATENT APPLICATION: US/09/673,605A TIME: 15:51:20

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L:35 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:36 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:60
L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:120
L:38 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:180
L:39 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:240
L:41 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:360
L:42 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:420
L:43 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:480
L:44 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:540
L:45 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:600
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:660
L:47 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:720
L:48\ M:341\ W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:780
L:49 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:840
L:50 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:900
L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:960
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1020
L:53 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1080
L:66 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:60
L:68 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:120
L:69 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:180
L:70 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:240
L:83 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:84 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:60
L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:120
L:86 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:180
L:87 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:240
L:88 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:300
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:360
L:90 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:420
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:480
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:540
L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:600
L:94 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:660
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:720
L:96 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:780
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:300
L:115 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:360
L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:420
L:117 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:480
L:118\ M:341\ W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:540
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:600
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:660
L:121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:720
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:780
L:135 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
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L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:60
L:137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:120
L:623 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:767 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:34
L:767 M:252 E: No. of Seq. differs, <211> LENGTH:Input:595 Found:576 SEQ:34
L:786 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:35
L:786 M:252 E: No. of Seq. differs, <211> LENGTH:Input:119 Found:96 SEQ:35
L:827 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:36
L:827 M:252 E: No. of Seq. differs, <211> LENGTH:Input:295 Found:272 SEQ:36
L:870 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:37
L:870 M:252 E: No. of Seq. differs, <211> LENGTH:Input:308 Found:288 SEQ:37
L:905 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:38
L:905 M:252 E: No. of Seq. differs, <211> LENGTH:Input:245 Found:224 SEQ:38
L:956 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:39
L:956 M:252 E: No. of Seq. differs, <211> LENGTH:Input:375 Found:352 SEQ:39
L:1029 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:40
L:1029 M:252 E: No. of Seq. differs, <211> LENGTH:Input:547 Found:528 SEQ:40
L:1104 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:41
L:1104 M:252 E: No. of Seq. differs, <211> LENGTH:Input:566 Found:544 SEQ:41
L:1159 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:42
L:1159 M:252 E: No. of Seq. differs, <211> LENGTH:Input:406 Found:384 SEQ:42
L:1200 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:43
L:1200 M:252 E: No. of Seq. differs, <211> LENGTH:Input:290 Found:272 SEQ:43
L:1228 M:252 E: No. of Seq. differs, <211> LENGTH:Input:185 Found:160 SEQ:44
L:1267 M:252 E: No. of Seq. differs, <211> LENGTH:Input:274 Found:256 SEQ:45
L:1293 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:46
L:1293 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1293 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:1293 M:252 E: No. of Seq. differs, <211> LENGTH:Input:172 Found:171 SEQ:46
L:1430 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:47
M:332 Repeated in SeqNo=47
L:1443 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1161 Found:1136 SEQ:47
L:1462 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:48
L:1462 M:252 E: No. of Seq. differs, <211> LENGTH:Input:115 Found:96 SEQ:48
L:1484 M:360 E: Sequence data overflow, line data truncated, for SEQ ID#:49
L:1484 M:252 E: No. of Seq. differs, <211> LENGTH:Input:141 Found:112 SEQ:49
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